RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/681, 878β_
Source: _1Fw/6_
Date Processed by STIC: _7/5/06_

ENTERED

RAW SEQUENCE LISTING   DATE: 07/05/2006
PATENT APPLICATION: US/10/681,878B   TIME: 14:22:51

Input Set : **A:\44463336.APP**
Output Set: **N:\CRF4\07052006\J681878B.raw**

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 3 <110> APPLICANT: CHIANG, VINCENT L.
 4        CARRAWAY, DANIEL T.
 5        SMELTZER, RICHARD H.
 7 <120> TITLE OF INVENTION: PRODUCTION OF SYRINGYL LIGNIN IN GYMNOSPERMS
 9 <130> FILE REFERENCE: 044463-0336
11 <140> CURRENT APPLICATION NUMBER: 10/681,878B
12 <141> CURRENT FILING DATE: 2003-10-09
14 <150> PRIOR APPLICATION NUMBER: 09/796,256
15 <151> PRIOR FILING DATE: 2001-02-28
17 <150> PRIOR APPLICATION NUMBER: 08/991,677
18 <151> PRIOR FILING DATE: 1997-12-16
20 <150> PRIOR APPLICATION NUMBER: 60/033,381
21 <151> PRIOR FILING DATE: 1996-12-16
23 <160> NUMBER OF SEQ ID NOS: 24
25 <170> SOFTWARE: PatentIn Ver. 3.3
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1708
29 <212> TYPE: DNA
30 <213> ORGANISM: Liquidambar styraciflua
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33 <221> NAME/KEY: CDS
34 <222> LOCATION: (48)..(1571)
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38                                                         Met Ala Phe
39                                                          1
41 ctt cta ata ccc atc tca ata atc ttc atc gtc tta gct tac cag ctc   104
42 Leu Leu Ile Pro Ile Ser Ile Ile Phe Ile Val Leu Ala Tyr Gln Leu
43       5              10              15
45 tat caa cgg ctc aga ttt aag ctc cca ccc ggc cca cgt cca tgg ccg   152
46 Tyr Gln Arg Leu Arg Phe Lys Leu Pro Pro Gly Pro Arg Pro Trp Pro
47  20              25              30                      35
49 atc gtc gga aac ctt tac gac ata aaa ccg gtg agg ttc cgg tgt ttc   200
50 Ile Val Gly Asn Leu Tyr Asp Ile Lys Pro Val Arg Phe Arg Cys Phe
51               40              45              50
53 gcc gag tgg tca caa gcg tac ggt ccg atc ata tcg gtg tgg ttc ggt   248
54 Ala Glu Trp Ser Gln Ala Tyr Gly Pro Ile Ile Ser Val Trp Phe Gly
55           55              60              65
57 tca acg ttg aat gtg atc gta tcg aat tcg gaa ttg gct aag gaa gtg   296
58 Ser Thr Leu Asn Val Ile Val Ser Asn Ser Glu Leu Ala Lys Glu Val
59           70              75              80
61 ctc aag gaa aaa gat caa caa ttg gct gat agg cat agg agt aga tca   344
62 Leu Lys Glu Lys Asp Gln Gln Leu Ala Asp Arg His Arg Ser Arg Ser
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63       85                      90                      95
65 gct gcc aaa ttt agc agg gat ggg cag gac ctt ata tgg gct gat tat     392
66 Ala Ala Lys Phe Ser Arg Asp Gly Gln Asp Leu Ile Trp Ala Asp Tyr
67 100                     105                     110                     115
69 gga cct cac tat gtg aag gtt aca aag gtt tgt acc ctc gag ctt ttt     440
70 Gly Pro His Tyr Val Lys Val Thr Lys Val Cys Thr Leu Glu Leu Phe
71                 120                     125                     130
73 act cca aag cgg ctt gaa gct ctt aga ccc att aga gaa gat gaa gtt     488
74 Thr Pro Lys Arg Leu Glu Ala Leu Arg Pro Ile Arg Glu Asp Glu Val
75                 135                     140                     145
77 aca gcc atg gtt gag tcc att ttt aat gac act gcg aat cct gaa aat     536
78 Thr Ala Met Val Glu Ser Ile Phe Asn Asp Thr Ala Asn Pro Glu Asn
79             150                     155                     160
81 tat ggg aag agt atg ctg gtg aag aag tat ttg gga gca gta gca ttc     584
82 Tyr Gly Lys Ser Met Leu Val Lys Lys Tyr Leu Gly Ala Val Ala Phe
83         165                     170                     175
85 aac aac att aca aga ctc gca ttt gga aag cga ttc gtg aat tca gag     632
86 Asn Asn Ile Thr Arg Leu Ala Phe Gly Lys Arg Phe Val Asn Ser Glu
87 180                     185                     190                     195
89 ggt gta atg gac gag caa gga ctt gaa ttt aag gaa att gtg gcc aat     680
90 Gly Val Met Asp Glu Gln Gly Leu Glu Phe Lys Glu Ile Val Ala Asn
91                 200                     205                     210
93 gga ctc aag ctt ggt gcc tca ctt gca atg gct gag cac att cct tgg     728
94 Gly Leu Lys Leu Gly Ala Ser Leu Ala Met Ala Glu His Ile Pro Trp
95             215                     220                     225
97 ctc cgt tgg atg ttc cca ctt gag gaa ggg gcc ttt gcc aag cat ggg     776
98 Leu Arg Trp Met Phe Pro Leu Glu Glu Gly Ala Phe Ala Lys His Gly
99             230                     235                     240
101 gca cgt agg gac cga ctt acc aga gct atc atg gaa gag cac aca ata    824
102 Ala Arg Arg Asp Arg Leu Thr Arg Ala Ile Met Glu Glu His Thr Ile
103         245                     250                     255
105 gcc cgt aaa aag agt ggt gga gcc caa caa cat ttc gtg gat gca ttg    872
106 Ala Arg Lys Lys Ser Gly Gly Ala Gln Gln His Phe Val Asp Ala Leu
107 260                     265                     270                     275
109 ctc acc cta caa gag aaa tat gac ctt agc gag gac act att att ggg    920
110 Leu Thr Leu Gln Glu Lys Tyr Asp Leu Ser Glu Asp Thr Ile Ile Gly
111                 280                     285                     290
113 ctc ctt tgg gat atg atc act gca ggc atg gac aca acc gca atc tct    968
114 Leu Leu Trp Asp Met Ile Thr Ala Gly Met Asp Thr Thr Ala Ile Ser
115             295                     300                     305
117 gtc gaa tgg gcc atg gcc gag tta att aag aac cca agg gtg caa caa    1016
118 Val Glu Trp Ala Met Ala Glu Leu Ile Lys Asn Pro Arg Val Gln Gln
119             310                     315                     320
121 aaa gct caa gag gag cta gac aat gta ctt ggg tcc gaa cgt gtc ctg    1064
122 Lys Ala Gln Glu Glu Leu Asp Asn Val Leu Gly Ser Glu Arg Val Leu
123         325                     330                     335
125 acc gaa ttg gac ttc tca agc ctc cct tat cta caa tgt gta gcc aag    1112
126 Thr Glu Leu Asp Phe Ser Ser Leu Pro Tyr Leu Gln Cys Val Ala Lys
127 340                     345                     350                     355
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129 gag gca cta agg ctg cac cct cca aca cca cta atg ctc cct cat cgc   1160
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131             360                 365                 370
133 gcc aat gcc aac gtc aaa att ggt ggc tac gac atc cct aag gga tca   1208
134 Ala Asn Ala Asn Val Lys Ile Gly Gly Tyr Asp Ile Pro Lys Gly Ser
135             375                 380                 385
137 aat gtt cat gta aat gtc tgg gcc gtg gct cgt gat cca gca gtg tgg   1256
138 Asn Val His Val Asn Val Trp Ala Val Ala Arg Asp Pro Ala Val Trp
139             390                 395                 400
141 cgt gac cca cta gag ttt cga ccg gaa cgg ttc tct gaa gac gat gtc   1304
142 Arg Asp Pro Leu Glu Phe Arg Pro Glu Arg Phe Ser Glu Asp Asp Val
143     405                 410                 415
145 gac atg aaa ggt cac gat tat agg cta ctg ccg ttt ggt gca ggg agg   1352
146 Asp Met Lys Gly His Asp Tyr Arg Leu Leu Pro Phe Gly Ala Gly Arg
147 420                 425                 430                 435
149 cgt gtt tgc ccc ggt gca caa ctt ggc atc aat ttg gtc aca tcc atg   1400
150 Arg Val Cys Pro Gly Ala Gln Leu Gly Ile Asn Leu Val Thr Ser Met
151             440                 445                 450
153 atg ggt cac cta ttg cac cat ttc tat tgg agc cct cct aaa ggt gta   1448
154 Met Gly His Leu Leu His His Phe Tyr Trp Ser Pro Pro Lys Gly Val
155             455                 460                 465
157 aaa cca gag gag att gac atg tca gag aat cca gga ttg gtc acc tac   1496
158 Lys Pro Glu Glu Ile Asp Met Ser Glu Asn Pro Gly Leu Val Thr Tyr
159             470                 475                 480
161 atg cga acc ccg gtg caa gct gtt ccc act cca agg ctg cct gct cac   1544
162 Met Arg Thr Pro Val Gln Ala Val Pro Thr Pro Arg Leu Pro Ala His
163     485                 490                 495
165 ttg tac aaa cgt gta gct gtg gat atg taattcttag tttgttatta         1591
166 Leu Tyr Lys Arg Val Ala Val Asp Met
167 500                 505
169 ttcatgctct taaggttttg gactttgaac ttatgatgag atttgtaaaa ttccaagtga 1651
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174 <210> SEQ ID NO: 2
175 <211> LENGTH: 508
176 <212> TYPE: PRT
177 <213> ORGANISM: Liquidambar styraciflua
179 <400> SEQUENCE: 2
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183 Tyr Gln Leu Tyr Gln Arg Leu Arg Phe Lys Leu Pro Pro Gly Pro Arg
184             20                  25                  30
186 Pro Trp Pro Ile Val Gly Asn Leu Tyr Asp Ile Lys Pro Val Arg Phe
187         35                  40                  45
189 Arg Cys Phe Ala Glu Trp Ser Gln Ala Tyr Gly Pro Ile Ile Ser Val
190     50                  55                  60
192 Trp Phe Gly Ser Thr Leu Asn Val Ile Val Ser Asn Ser Glu Leu Ala
193 65                  70                  75                  80
195 Lys Glu Val Leu Lys Glu Lys Asp Gln Gln Leu Ala Asp Arg His Arg
196             85                  90                  95
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198 Ser Arg Ser Ala Ala Lys Phe Ser Arg Asp Gly Gln Asp Leu Ile Trp
199         100             105             110
201 Ala Asp Tyr Gly Pro His Tyr Val Lys Val Thr Lys Val Cys Thr Leu
202         115             120             125
204 Glu Leu Phe Thr Pro Lys Arg Leu Glu Ala Leu Arg Pro Ile Arg Glu
205     130             135             140
207 Asp Glu Val Thr Ala Met Val Glu Ser Ile Phe Asn Asp Thr Ala Asn
208 145             150             155             160
210 Pro Glu Asn Tyr Gly Lys Ser Met Leu Val Lys Lys Tyr Leu Gly Ala
211             165             170             175
213 Val Ala Phe Asn Asn Ile Thr Arg Leu Ala Phe Gly Lys Arg Phe Val
214         180             185             190
216 Asn Ser Glu Gly Val Met Asp Glu Gln Gly Leu Glu Phe Lys Glu Ile
217         195             200             205
219 Val Ala Asn Gly Leu Lys Leu Gly Ala Ser Leu Ala Met Ala Glu His
220     210             215             220
222 Ile Pro Trp Leu Arg Trp Met Phe Pro Leu Glu Glu Gly Ala Phe Ala
223 225             230             235             240
225 Lys His Gly Ala Arg Arg Asp Arg Leu Thr Arg Ala Ile Met Glu Glu
226             245             250             255
228 His Thr Ile Ala Arg Lys Lys Ser Gly Gly Ala Gln Gln His Phe Val
229             260             265             270
231 Asp Ala Leu Leu Thr Leu Gln Glu Lys Tyr Asp Leu Ser Glu Asp Thr
232         275             280             285
234 Ile Ile Gly Leu Leu Trp Asp Met Ile Thr Ala Gly Met Asp Thr Thr
235     290             295             300
237 Ala Ile Ser Val Glu Trp Ala Met Ala Glu Leu Ile Lys Asn Pro Arg
238 305             310             315             320
240 Val Gln Gln Lys Ala Gln Glu Glu Leu Asp Asn Val Leu Gly Ser Glu
241             325             330             335
243 Arg Val Leu Thr Glu Leu Asp Phe Ser Ser Leu Pro Tyr Leu Gln Cys
244         340             345             350
246 Val Ala Lys Glu Ala Leu Arg Leu His Pro Pro Thr Pro Leu Met Leu
247         355             360             365
249 Pro His Arg Ala Asn Ala Asn Val Lys Ile Gly Gly Tyr Asp Ile Pro
250     370             375             380
252 Lys Gly Ser Asn Val His Val Asn Val Trp Ala Val Ala Arg Asp Pro
253 385             390             395             400
255 Ala Val Trp Arg Asp Pro Leu Glu Phe Arg Pro Glu Arg Phe Ser Glu
256             405             410             415
258 Asp Asp Val Asp Met Lys Gly His Asp Tyr Arg Leu Leu Pro Phe Gly
259         420             425             430
261 Ala Gly Arg Arg Val Cys Pro Gly Ala Gln Leu Gly Ile Asn Leu Val
262         435             440             445
264 Thr Ser Met Met Gly His Leu Leu His His Phe Tyr Trp Ser Pro Pro
265     450             455             460
267 Lys Gly Val Lys Pro Glu Glu Ile Asp Met Ser Glu Asn Pro Gly Leu
268 465             470             475             480
270 Val Thr Tyr Met Arg Thr Pro Val Gln Ala Val Pro Thr Pro Arg Leu
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279 <211> LENGTH: 1883
280 <212> TYPE: DNA
281 <213> ORGANISM: Liquidambar styraciflua
283 <220> FEATURE:
284 <221> NAME/KEY: CDS
285 <222> LOCATION: (74)..(1606)
287 <400> SEQUENCE: 3
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290 agagagagaa gcc atg gat tct tct ctt cat gaa gcc ttg caa cca cta     109
291             Met Asp Ser Ser Leu His Glu Ala Leu Gln Pro Leu
292              1               5                  10
294 ccc atg acg ctg ttc ttc att ata cct ttg cta ctc tta ttg ggc cta  157
295 Pro Met Thr Leu Phe Phe Ile Ile Pro Leu Leu Leu Leu Gly Leu
296          15                  20                  25
298 gta tct cgg ctt cgc cag aga cta cca tac cca cca ggc cca aaa ggc  205
299 Val Ser Arg Leu Arg Gln Arg Leu Pro Tyr Pro Pro Gly Pro Lys Gly
300      30                  35                  40
302 tta ccg gtg atc gga aac atg ctc atg atg gat caa ctc act cac cga  253
303 Leu Pro Val Ile Gly Asn Met Leu Met Met Asp Gln Leu Thr His Arg
304  45                  50                  55                  60
306 gga ctc gcc aaa ctc gcc aaa caa tac ggc ggt cta ttc cac ctc aag  301
307 Gly Leu Ala Lys Leu Ala Lys Gln Tyr Gly Gly Leu Phe His Leu Lys
308              65                  70                  75
310 atg gga ttc tta cac atg gtg gcc gtt tcc aca ccc gac atg gct cgc  349
311 Met Gly Phe Leu His Met Val Ala Val Ser Thr Pro Asp Met Ala Arg
312              80                  85                  90
314 caa gtc ctt caa gtc caa gac aac atc ttc tcg aac cgg cca gcc acc  397
315 Gln Val Leu Gln Val Gln Asp Asn Ile Phe Ser Asn Arg Pro Ala Thr
316          95                  100                 105
318 ata gcc atc agc tac ctc acc tat gac cga gcc gac atg gcc ttc gct  445
319 Ile Ala Ile Ser Tyr Leu Thr Tyr Asp Arg Ala Asp Met Ala Phe Ala
320      110                 115                 120
322 cac tac ggc ccg ttt tgg cgt cag atg cgt aaa ctc tgc gtc atg aaa  493
323 His Tyr Gly Pro Phe Trp Arg Gln Met Arg Lys Leu Cys Val Met Lys
324 125                 130                 135                 140
326 tta ttt agc cgg aaa cga gcc gag tcg tgg gag tcg gtc cga gac gag  541
327 Leu Phe Ser Arg Lys Arg Ala Glu Ser Trp Glu Ser Val Arg Asp Glu
328              145                 150                 155
330 gtc gac tcg gca gta cga gtg gtc gcg tcc aat att ggg tcg acg gtg  589
331 Val Asp Ser Ala Val Arg Val Val Ala Ser Asn Ile Gly Ser Thr Val
332          160                 165                 170
334 aat atc ggc gag ctg gtt ttt gct ctg acg aag aat att act tac agg  637
335 Asn Ile Gly Glu Leu Val Phe Ala Leu Thr Lys Asn Ile Thr Tyr Arg
336          175                 180                 185
338 gcg gct ttt ggg acg atc tcg cat gag gac cag gac gag ttc gtg gcc  685
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 07/05/2006

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:21; Xaa Pos. 3,5,6,8

Seq#:22; N Pos. 23

VERIFICATION SUMMARY   DATE: 07/05/2006
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Input Set : **A:\44463336.APP**
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L:1259 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0
L:1278 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0